

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Lavi, Sara
- (ii) TITLE OF INVENTION: MANIPULATION AND DETECTION OF PROTEIN
PHOSPHATASE 2C -PP2CALPHA- EXPRESSION IN TUMOR CELLS FOR
CANCER THERAPY, PREVENTION AND DETECTION
- (iii) NUMBER OF SEQUENCES: 20
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Kohn & Associates
(B) STREET: 30500 Northwestern Hwy.
(C) CITY: Farmington Hills
(D) STATE: Michigan
(E) COUNTRY: US
(F) ZIP: 48334
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Kohn, Kenneth I.
(B) REGISTRATION NUMBER: 30,955
(C) REFERENCE/DOCKET NUMBER: 2290.00037
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Asp | Asp | Thr | Asp | Ser | Ala | Ser | Thr | Asp |
| 1 | | | | | 5 | | | | 10 |

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids

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- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Tyr	Lys	Asn	Asp	Asp	Thr	Asp	Ser	Thr	Ser	Thr	Asp	Asp	Met	Trp
1				5				10					15	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Pro	Asn	Lys	Asp	Asn	Asp	Gly	Gly	Ala
1				5				

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGGATCAAGT CATAATGGGA

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 - (A) DESCRIPTION: /desc = "Primer"

(iv) ANTI-SENSE: YES

GCTGGAGTCT GATTACAAC

20

(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "Primer"

GAAGTAGTCG ACACCTGT

18

(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "Primer"

GTTTGAGACC TTCAACACCC C

21

(D) TOPOLOGY: linear

(A) DESCRIPTION: /desc = "Primer"

GTGGCCATCT CTTGCTCGAA GTC

23

(B) TYPE: amino acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Gly Ala Phe Leu Asp
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGGGATCCGC ATGGGAGCAT TTTTAGAC

28

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Thr Asp Asp Met Trp
1 5

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 27 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "Primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CGCGGATCCT TACCACATAT CATCAGT

27

Sequence = 5'-TGGTGG-3'

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 64 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Silencer Region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ACTCCATCAC TAGGGGTTCC TGGAGGGGTG GAGTCGTGAC GTGAATTACG TCATAGGGTT 60
 AGGG 64

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "Mini-silencer region"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

ACTCCCATCA CTAGGGGTTC CT 22

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1573 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "35-3.seg (Figure 3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAGCTTGTC A AATTACTAT TCAGTGTGAT TTTTAGTGGA TGAAACCTCA TGACTAGTAT 60
 ATTATGACAT TAGCTTTGCG TAGTGAAGGC ACAAGCTGCT AAGTGTTAG GGATGTATTT 120
 TGCCGTAGCC TGTATCACNC CAGGTCCTGG GCTCGGTTCC TAGCATTACA GGAAAAAGCA 180
 GGCGGTGGTT GACCTTTAAT GAATGGATTT TTCAATTTAG AAGTTGGTTT CATTTTAAAG 240
 AATTCAAAAA TGTTCCCAT AGCACTTTGT TTTGACATTG AGATCAGCTG CTAATTGAGG 300
 TCCAGTATAT ACTTAGAAAA CTGAGCGAAA CTTTGATGGA CACACACACA CACCCCTGTT 360
 GTTCATTTAA TAATTGAACT AAATAAAATA CTGTTTAGTC ATCCACGTAA GCAAGAGGCC 420

TGTGTAAACA GTATTTGTAT TAGTAAAAAC TTTATAACAT AGTTACATAA TCAGCATCAT 480
 TTTTTTTATG GACCTTATAG TTGGCTACTT CACTGGGTTT GTTATAATTT AATCAGACTC 540
 CTAAATAGGT TAAATTTCTG AATTGCCTAC TTCAGTTTTG AAGAATTATT TTGTTTCATA 600
 ATTTCCCATG CATATCTGGT AAATAATTCT GGATTGTTTC TAAAGGGGAG AGCAAGGTCT 660
 CTTATGCAAA GTGAAATCT AGATATGCTG TTTGTAAGAA TATAATAGTG ATAAAGTAGT 720
 GTCCTTTTGC TCAGTGCCTC CATTCTTACC AGGCTGTGAC TGATCTTCAG TATTATTCAG 780
 ACAGTCACTA TTAATATATC CGTTGCACAG TGGGGAAATT GAGGGAAAGT AGATAGGCAT 840
 CGGGTATCTT AATCATAACT CACATATACC CAGCTGGCTA GTCAGCCTAG CTAAGACAGT 900
 TCACACCCAG TTGAGGCAGC TTGCTGTTGG CCATTAGTAG GTAACCTAAT GGCTTGGTTT 960
 CTTCACTGGT AAGGTGGGGA TATAATAATG CCAATAATTG CATAATGATT AAAGACATTA 1020
 ATATATTCCA TAAAATTTCC TGAATAGTGC TTAGCTGGTA CCCCTCCCCA CACATGCACC 1080
 CCAGTCCAAT GTTCAGATGT TTACTTTGTT AAGCCCAGTT AATCCATTCC CCCTAATATC 1140
 TTCTCCCAGT TTGAAGAANG TTGAAGAATG TTGGGCTTGT TAGTTTAATT TTTTAAGAAG 1200
 CATATCATGT TGCTTTTTTA AAACATGTTT CTTTGGGTTT TGGCTTCCCC TTTTGAAAG 1260
 AATTCCAATT TACACTTATG GAAGAAAGCC ATTGTCCCTT CCAATTTCCC CCCCTGTCCC 1320
 TTCCAATAC AGCCCAACTC CCCATGTTTT GACTTCCTCC CCTGAACCAC CCCGTTCTCC 1380
 TGTTTTTCCC TCCCCANAA AAAAAACCA ATAATTTGAC TTTGGTAATT GAATTTCCCG 1440
 CCNGTTAGGC NCCTGAATTG CCGAAATAAT TCCCCGTGC NCCNGGANT TTTGGCACCC 1500
 CCTGCCCCCTT AACCTGTTCT GCTGCCCCC ATTTTAAAT GGCTTGCCGC NTTACNCAA 1560
 ANACTGCCTT TCC 1573

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "35-T7.seg (Figure 3)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTCGATCTCA CAAAGTCACA GAGCTCTTCG TTTCCCATGA CATCCCAGAT ACCATCACAT 60
 GCAAGAATAA TGAAGTATC GTCCTCTTCA GACCTTTCAA TATCATGGAC TTCTGGCTCT 120
 GGTGAGACGA GCTGCTCTGT GGGACCTTTT CCATGGACAC ATTTGTAATC GAAATCCCCA 180
 AGGGCCCTTG ACACAGCCAG AGAGCCATTT ACACGCTGAA TCATCACAGA GCCCCCTGCA 240
 TTCTGAATTC GTTCTTTTTT CAGCGGGTTA CTTGGTTTGT GGTCTTGTGT GAAGAAGTGA 300

ACTTTCCTGT	TTCTACAAAG	CAAACCTCTC	GAGTCTCCAC	AGTTAATGAA	GTAAGTATGT	360
TTGGGGAGAA	ATTAAGACCC	CCACAGCTGT	TTGACCCACT	TCCTATCTGC	ACCATGTTTT	420
CCTTCCTCCT	GACATGACTC	CTCATGTTGT	TTCCATCAAT	CTCCCAGAAA	AACCTGTTCC	480
TGATCCCCAT	TCCTTTACAT	TTTCCCACAG	AAAGGTGCTC	CCTGCAGAGC	CTTTTAAAAAT	540
CCCTGGTTTA	TTGGTGATGT	TGATTCTNAA	CAAATGCTCC	ACAGCCAGTA	TTTNGGCAAC	600
CTTGAAAAAC	CAGCATGCCC	ATCCATATAC	AGCCAAGAAT	GACCATGTTC	TCCAGTTCCA	660
CTTTNGGCAA	ACCCAATCCA	CAGCCGTTNT	GCGCATCCTC	CCATTTCAAC	TCCGCCCAAC	720
CNTTGCNTGC	TGCNTTAAGC	CATATCGCAA	CCCATCCCCC	CTGCCCCCTG	GGGCATTATG	780
CNTTTCCATC	TTTGGTTGTC	TAAAAATGCTC	CCATTATGAC	TTGATCCTCT	AGGTCTGCAA	840
AGGAAGAGAA	ATAAGAAAGT	TAGTAACTGT	CTTTGAAACA	AAGCACACAT	CCAACAGTCT	900
TTTTGAAGCA	CCTACGAGAT	ACAAGGAAAC	GTAAAACTC	ATAGGCTATA	GCCATAAGCA	960
TTGTTCTACT	GACTTGGAAG	ATGTAGAGAT	TAATAAGAAA	GGGAAAGGCT	GATCAAGTAC	1020
AGCTCAACCA	GACAAGCAGC	AGATGGAAGT	AAGTCACCAG	GTAAAAGAGA	GCTTGTGTTG	1080
CTCTCTGTGA	TACCAAGGAG	GCCCAGCAGT	GACCATTAAAC	TTACATGAAC	TAGGCAAGAT	1140
TTCAGGGTGC	ATTCATCATA	TGTAACCTCT	CAATTAAAGT	GTGTGTTGAT	TAAAAAAAAT	1200
AATTCATAGA	AACATACAAG	TATCTACTAC	TTCAGGGAAC	CTTAGCTAAG	TACTCAGGAA	1260
TGTTGAGAGT	TTGATTCCAT	GCTATTTAGT	TTTGTCTCTA	CAACTAGATA	CCTTTGGTAA	1320
AAATAAAAAG	TAATTACTCA	CACTGGTCCA	AATTTTCAGT	GCCTTGTCGA	GGTCATTCTC	1380
TTTAGCTGGA	ATTCCTTGCC	TCACCTCTTT	ACCAACAGAA	AAAAAATACA	CCTGTTTCTA	1440
TCCTTTGAAA	TCCAGTTCAA	TTGTTCCCCC	TTCTCCAGA	CTTTACAGTC	CTTGAAAAAA	1500
ACAAGTTATT	AACTACAGAA	GTCAGCTTCC	ATTTCAGTT	NGGAATGTTT	TTTAATGAAC	1560
AATTTTATTG	TTCNAAATCT	NACNATATGA	TAAC TAANCN	AATGGTAATA	ATATTTTCAN	1620
CCCTGCCCTA	TGGCCGCTNT	TTTTAATCCT	NAAAAAAATC	NAAGGTCTAT	TCCNCCCNCC	1680
CTTGCCAATA	CTTNACANCN	CCAGTTCCCT	GATCTGGAAT	GGACCCACAA	AGGTCAAGAC	1740
TTAGGTTANC	CCTTGCTCAC	AAACTAAAGA	AAATCTTAAA	GGAGAACAGA	ATACTGAAGA	1800
GAGAAATGAG	GGTGAAGGAC	AGTGTTTCAGG	TGACGTTCTG	AAACCAGGGG	ACTAAANATA	1860
CCANAANTGG	TGTTNCAGAC	AGAAATGGTA	TGGAAAACTC	CTTAGGAAAG	AAATGACANN	1920
TNTTGTTTTG	CAGCAACCCC	CNCACATGGC	TTTCTCTTTT	TCCTTCTGCT	GATTAAGTGA	1980
TGCACNTGGT	ANAAAAGTCA	ACANACCCCT	CCTCCACNCA	GACTCCCACC	GAGTACANNG	2040
GCCCATGTGC	TCANTACACT	CTGCCCCAAA	CTCMNANNAT	TCATTNNCT	CCCCNTGTNA	2100
TTTATNAGGG	CCTTTCCCNT	CAGTTNTCTN	ATCNCCAACG	GANATTANCC	TTCCANNNAT	2160
TTACCCCCNN	TTGTACANNC	ACATNNTGGC	NNGTGCCACN	GTTANGCGTC	GGCNTCCCTG	2220
TNCACTNCA	TCCCTCATCN	TTAGGCCANG	TTTGATTCTC	CNGTGCANAN	TTTCCGCANN	2280

ANCNTACCCC	TTGCACCNTC	CATNTCTNNG	GAANAACCTC	CGGTTCTGAA	TCTNCCCCNN	2340
TCCCGTCNCT	CCCCNTTCT	TTCTTTTCTC	TANTTTTTTC	CNNGGNACGG	GTTGNGGTNA	2400
ATNAANNCCC	CTCCTTCGTC	TATTCANCCC	TTCCTATGNA	CACTTCCTGN	CCCCCTATCT	2460
CTCTATNTNC	TNCTCTCTAT	ATCTNNATCC	CNTCTTCNCN	TGCCNCTCCC	TNGTNTTNNA	2520
NCGGGTATTT	NTNTTCTCC	TCNTCTTCTT	CCCCTNTNTA	NCCNTNCTNC	NNNCNNNCCC	2580

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 830 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "5H-1 (Example 10)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TGGGGGAGAG	GA CTGAAATA	TTTCCACAGC	CTTTTTATTG	GTGGTGATGG	TAGTGATGGT	60
TAGGATTCCT	TCTTTCCTTC	TTTCTTTCTT	TCTTTCCTTC	TTTCTTTTTT	TTTTTTTTTT	120
TTTTTTTTTT	GAGACAGGGT	TTCTCTGGGT	ACTCCTGGAA	CTCACTTTGT	GGACCATGAA	180
TGACATGAAT	ACTTCGATAT	ATACATACAT	ACAAAGACAC	ATATTTTTTAA	AAAGAGAATT	240
AGAGTAGAGC	TGGGGCAATT	GTGGAACACA	CCTTTAACCT	CAGGCAGATT	TCTGCGTTCA	300
AGGTCACCTT	GGATTACAAG	GCAGCTAGGG	CTACACAGAG	AAACCATATC	TCAAAAAAAAA	360
GAAAAAATAA	TGAAAGAAAG	AAAGGAAGGA	AGGAAGGAAG	GAAGGAAGGA	AGGAAGGAAG	420
AAAGGAAGGT	AGGAAGAAAG	GTATTTTCCT	AAAAAAAAAA	AAAAAAAAAA	TTTATTCCGG	480
GCA GTGGTGG	CAATGCTTT	TAATCCCACC	ATTTGGGAAA	GCAGAGGCAG	ACAGATTAA	540
TTTTCAAGGC	CCACCTGGTC	CTACACAGTG	AATTCCAGGA	ACACCTAGGT	TTACCCANAA	600
AAAACCCCC	CTTGAAATAA	ACAAAAATAA	ATTAAATAAA	TAA AATT TAA	AAATAAAACC	660
CGGGCGTTAA	ACCCNCTTTT	ATCCCCCACC	TTNGGAAGCA	AAAGCCGGCN	GATTTCTGAA	720
TTCNAGGCCN	CCCTGTCTAT	GAATTANTTC	CCNGAACACC	CNAATTTTTC	NAAAAACCCC	780
CCNTTCTTA	AAAAANCCAA	ATTATTATTN	ATTAATTA	TTAAATTACC		830

(2) INFORMATION FOR SEO ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 838 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "AN8T7 (Example 10)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

GGAGTCCAAC AATGGTTTCC ACTTGTCTGG CGGCCGCTCT AGAGTTTCCC ATAAGCTGGA 60
CTGAGAGATG GTGTGATTGC TGTGGGTGAC AAAGACAGAG GCACCTTTCA TCTCTACCTT 120
TCTCTTGTTT TGTGTTTGT TTGAGACCGG TTCCCACTAT GTAGACCAGG CTGGAGGACA 180
GGGTCTCACT ATGTAGACCA GGCTGGCCTT GAACTCAAAG ACATCTGCCT GCCTCTGCCT 240
CCTGAGGGCT GGGATTAAAG GCGTGTGCTG CCACTGACAG CTTCATCCTT CCTGTCTATCA 300
GTCCCGGCTC ACAGGGCCAG AAGATCTCTT CTATGCTTCC ACTATTTCCC CAATCCATTC 360
CCACGGCAGC CTCTCCATCT CCCTACCACC AAGACAGCAG CCTAGTGATA TAACAAAAC 420
TTTATTACACA GGAAACCGGA AAACAAAATC ACAACCAATC ATTTCTATCT AGTCCCTGCC 480
CTAGCCCTCC CTCCAAGCCC CTACATATCC TCCATCTGAG GGGGATGCAT GCGTTGGGTG 540
GGAGCTGCCG GCATCCTTAT CCTGGTTCCT GGAGTAGNGA AGAGTGGTTC TTTTCAACGN 600
CTAGGGNNCT CCCCTCCAAG TTNGGACCTC TCTTCCCAGG NCTTCNCCCC TCCCTNACAG 660
GGNACAAAAA ACCAGGNACG GCACNACGCC AGGNAGGAAG GGACTCTTGG NAATGTTGGG 720
CAGGACTTGT CCTCAGAATT CCNNGGAGGA ATCAAGGGCC TTGAATTCGG GAACCACTNC 780
CGAGGNCTTC ANCANGGCAN AGTTCAATTT TCCATCCCAG TTGGCCCANCT CTGGCCNG 838

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "CHINT (TABLE 5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TAGTGCCGGT CAAGGAACTG AACGTGCGAT TCCGGGACAG GCTACCCACT CCGATCCCAG 60
GAGAAGTTGT CATGGTGAGG GCCACCCTAG GTCTCTGCCC CTGCTGTGTC CCCCATCTTA 120
CCCATCCAGT AGGATCTAGA GGCTGTCGCC CCCTTGTTGA ATGCACAGAA GTCACAAGCG 180

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "HUMMDB (TABLE 5)"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CCTCACCTCC GCCCTGTTTC GTCCAGGTCC TCCGGGTCAG GCTACCCCCG TCGCCGCCAG	60
AGCGCGGGGG AGGGGAGAGC TTCCTTTGTC TCCTATGCCT CCTCCCCCCA TCCGGGCTCT	120
CCTGCGGGCA AGCGCCGAGG GGACACCGGG GAGTACCCA CCTGAACCTC TGGGG	175

Sequence